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29.	Adamowicz, et al., "Nutritional complementation of oxidative glucose metabolism in <i>Escherichia coli</i> via pyrroloquinoline quinone-dependent glucose dehydrogenase and the Entner-Doudoroff pathway," <i>Appl Environ Microbiol</i> , 57(7):2012-2015 (1991).
30.	Alberty, "Calculation of Biochemical Net Reactions and Pathways by Using Matrix Operations," <i>Biophys J</i> , 71(1):507-515 (1996).
31.	Alm, et al., "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen <i>Helicobacter pylori</i> ," <i>Nature</i> , 397(6715):176-80 (1999).
32.	Aloni, et al., "Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays," <i>Proc Natl Acad Sci U.S.A.</i> , 96(12):6745-6750 (1999).
33.	Alter, et al., "Singular value decomposition for genome-wide expression data processing and modeling," <i>Proc Natl Acad Sci U.S.A.</i> , 97(18):10101-10106 (2000).
34.	Altschul, et al., "Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs," <i>Nucl Acids Res</i> , 25(17):3389-3402 (1997).
35.	Alves, et al., "Systemic properties of ensembles of metabolic networks: application of graphical and statistical methods to simple unbranched pathways," <i>Bioinformatics</i> , 16(6):534-547 (2000).
36.	Andre, "An overview of membrane transport proteins in <i>Saccharomyces cerevisiae</i> ," <i>Yeast</i> , 11(16):1575-1611 (1995).
37.	Anonymous, "The yeast genome directory" <i>Nature</i> , 387(6632 Suppl):5 (1997).
38.	Appel, et al., "A new generation of information retrieval tools for biologists: the example of the ExPASy WWW server," <i>Trends Biochem Sci</i> , 19(6):258-260 (1994).
39.	Attanoos, et al., "Ileostomy polyps, adenomas, and adenocarcinomas," <i>Gut</i> , 37(6):840-844 (1995).
40.	Baba, et al., "Construction of <i>Escherichia coli</i> K-12 in-frame, single-gene knockout mutants: the Keio collection," <i>Mol Syst Biol</i> , 2:2006-2008 (2006).
41.	Bailey, "Complex Biology With No Parameters," <i>Nat Biotechnol</i> , 19(6):503-504 (2001).
42.	Bailey, TL and Elkan, C, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers," <i>Proc Int Conf Intell Syst Mol Biol</i> , 2:28-36 (1994).
43.	Bailey, TL and Gribskov, M, "Combining evidence using p-values: application to sequence homology searches," <i>Bioinformatics</i> , 14(1):48-54 (1998).
44.	Bairoch, A, and Apweiler, R, "The SWISS-PROT Protein Sequence database and its supplement TrEMBL in 2000," <i>Nucleic Acids Res</i> , 28(1):45-48 (2000).
45.	Ball, et al., "Integrating functional genomic information into the <i>Saccharomyces</i> genome database," <i>Nucleic Acids Res</i> , 28(1):77-80 (2000).
46.	Ban, et al., "The mine and uracil catabolism in <i>Escherichia coli</i> ," <i>J Gen Microbiol</i> , 73(2):267-272 (1972).
47.	Bansal, "Integrating co-regulated gene-groups and pair-wise genome comparisons to automate reconstruction of microbial pathways," <i>Bioinformatics and Bioengineering Conference</i> , 209-216 (2001).
48.	Barclay, et al., "Sterol mutants of <i>Saccharomyces cerevisiae</i> : chromatographic analyses," <i>Lipids</i> , 12(8):645-654 (1977).
49.	Baxevas, "The Molecular Biology Database Collection: 2002 update," <i>Nucleic Acids Res</i> , 30:1-12 (2002).
50.	Beard, et al., "Energy Balance for Analysis of Complex Metabolic Networks," <i>Biophys J</i> , 83(1):79-86 (2002).

EXHIBIT A
U.S. Application No. 09/923,870

51.	Beckers, et al., "Large-Scale Mutational Analysis for the Annotation of the Mouse Genome," <u>Curr Opin Chem Biol</u> , 6(1):17-23 (2002).
52.	Bell, et al., "Composition and functional analysis of the <i>Saccharomyces cerevisiae</i> trehalose synthase complex," <u>J Biol Chem</u> , 273(50):33311-33319 (1998).
53.	Benson, et al., "GenBank," <u>Nucleic Acids Res</u> , 28(1):15-18 (2000).
54.	Berry, "Improving production of aromatic compounds in <i>Escherichia coli</i> by metabolic engineering," <u>Trends Biotechnol</u> , 14(7):250-256 (1996).
55.	Biale, "Living on the Edges," <u>Nat Biotechnol</u> , 19(2):111-112 (2001).
56.	Bianchi, P., and Zanella, A., "Hematologically Important Mutations: Red Cell Pyruvate Kinase (Third Update)," <u>Blood Cells, Molecules, and Diseases</u> , 15:47-53 (2000).
57.	Biaudet, et al., "Micado - a network-oriented database for microbial genomes," <u>Comput Appl Biosci</u> , 13(4):431-438 (1997).
58.	Birkholz, "Fumarate reductase of <i>Helicobacter pylori</i> --an immunogenic protein," <u>J Med Microbiol</u> , 41(1):56-62 (1994).
59.	Birner, et al., "Roles of phosphatidylethanolamine and of its several biosynthetic pathways in <i>Saccharomyces cerevisiae</i> ," <u>Mol Biol Cell</u> , 12(4):997-1007 (2001).
60.	Blackstock, WP and Wein, MP, "Proteomics: quantitative and physical mapping of cellular proteins," <u>Trends Biotechnol</u> , 17(3):121-127 (1999).
61.	BMES/EMBS Conference, Proceedings of the First Joint, Vol. 2, p. 1217 (1999).
62.	Bochner, "New technologies to assess genotype-phenotype relationships," <u>Nat Rev Genet</u> , 4(4):309-314 (2003).
63.	Boles, E, et al., "Identification and characterization of MAE 1, the <i>Saccharomyces cerevisiae</i> structural gene encoding mitochondrial malic enzyme," <u>J Bacteriol</u> , 180(11):2875-2882 (1998).
64.	Boles, et al., "A family of hexosephosphate mutases in <i>Saccharomyces cerevisiae</i> ," <u>Eur J Biochem</u> , 220(1):83-96 (1994).
65.	Boles, et al., "Characterization of a glucose-repressed pyruvate kinase (Pyk2p) in <i>Saccharomyces cerevisiae</i> that is catalytically insensitive to fructose-1,6-bisphosphate," <u>J Bacteriol</u> , 179(9):2987-2993 (1997).
66.	Bonarius, et al., "Metabolic flux analysis of hybridoma cells in different culture media using mass balances," <u>Biotechnol Bioeng</u> , 50(3):299-318 (1996).
67.	Bono, et al., "Reconstruction of amino acid biosynthesis pathways from the complete genome sequence," <u>Genome Research</u> , 8(3):203-210 (1998).
68.	Bottomley, et al., "Cloning, sequencing, expression, purification and preliminary characterization of a type II dehydroquinase from <i>Helicobacter pylori</i> ," <u>Biochem. J.</u> , 319(Pt 2):559-565 (1996).
69.	Bourot, S and Karst, F, "Isolation and characterization of the <i>Saccharomyces cerevisiae</i> SUT1 gene involved in sterol uptake," <u>Gene</u> , 165(1):97-102 (1995).
70.	Burgard, AP and Maranas, CD, "Probing the Performance Limits of the <i>Escherichia coli</i> Metabolic Network Subject to Gene Additions or Deletions," <u>Biotechnol Bioeng</u> , 74(5):364-375 (2001).
71.	Burgard, AP and Maranas, CD, "Review of the Enzymes and Metabolic Pathways (EMP) Database," <u>Metab Eng</u> , 3(3):193-194(2) (2001).
72.	Burgard, et al., "Minimal reaction sets for <i>Escherichia coli</i> metabolism under different growth requirements and uptake environments," <u>Biotechnol Prog</u> , 17(5):791-797 (2001).

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U.S. Application No. 09/923,870

73.	Burgard, et al., "Optkno: a bilevel programming framework for identifying gene knockout strategies for microbial strain optimization," <i>Biotechnol Bioeng</i> , 84(6):647-657 (2003).
74.	Burns, "Acetyl-CoA carboxylase activity in <i>Helicobacter pylori</i> and the requirement of increased CO ₂ for growth," <i>Microbiology</i> , 141(Pt 12):3113-3118 (1995).
75.	
76.	
77.	Chalker, et al., "Systematic identification of selective essential genes in <i>Helicobacter pylori</i> by genome prioritization and allelic replacement mutagenesis," <i>J Bacteriol</i> , 183(4):1259-1268 (2001).
78.	Chen, et al., "Characterization of the respiratory chain of <i>Helicobacter pylori</i> ," <i>FEMS Immunol Med Microbiol</i> , 24(2):169-174 (1999).
79.	Cherry, et al., "SGD: <i>Saccharomyces</i> Genome Database," <i>Nucleic Acids Res</i> , 26(1):73-79 (1998).
80.	
81.	Ciriacy, M and Breitenbach, I, "Physiological effects of seven different blocks in glycolysis in <i>Saccharomyces cerevisiae</i> ," <i>J Bacteriol</i> , 139(1):152-160 (1979).
82.	Clarke, "Complete set of steady states for the general stoichiometric dynamical system," <i>J Chem Phys</i> , 75(10):4970-4979 (1981).
83.	Clarke, "Stoichiometric network analysis," <i>Cell Biophys</i> , 12:237-253 (1988).
84.	
85.	Clifton, D and Fraenkel, DG, "Mutant studies of yeast phosphofructokinase," <i>Biochemistry</i> , 21(8):1935-1942 (1982).
86.	Clifton, et al., "Glycolysis mutants in <i>Saccharomyces cerevisiae</i> ," <i>Genetics</i> , 88(1):1-11 (1978).
87.	Compan, I and Touati, D, et al., "Anaerobic activation of <i>arcA</i> transcription in <i>Escherichia coli</i> : roles of Fnr and ArcA," <i>Mol Microbiol</i> , 11(5):955-964 (1994).
88.	Costanzo, et al., "YPD, PombePD and WormPD: model organism volumes of the BioKnowledge library, an integrated resource for protein information," <i>Nucleic Acids Res</i> , 29(1):75-9 (2001).
89.	Cotter, et al., "Aerobic regulation of cytochrome d oxidase (<i>cydAB</i>) operon expression in <i>Escherichia coli</i> : roles of Fnr and ArcA in repression and activation," <i>Mol Microbiol</i> , 25(3):605-615 (1997).
90.	
91.	Covert, et al., "Metabolic Modeling of Microbial Strains <i>In Silico</i> ," <i>Trends Biochem Sci</i> , 26(3):179-186 (2001).
92.	Covert, et al., "Regulation of Gene Expression in Flux Balance Models of Metabolism," <i>J Theor Biol</i> , 213(1):73-88 (2001).
93.	Covert, MW and Palsson, BO, "Constraints-based models: Regulation of Gene Expression Reduces the Steady-state Solution Space," <i>J Theor Biol</i> , 216 (2003).
94.	Covert, MW and Palsson, BO, "Transcriptional Regulation in Constraints-based Metabolic Models of <i>Escherichia coli</i> ," <i>J Biol Chem</i> , 277(31):28058- 28064 (2002).
95.	Copp, JR and McAlister-Henn, L, "Cloning and Characterization of the gene encoding the IDH1 subunit of NAD(+) dependent isocitrate dehydrogenase from <i>Saccharomyces cerevisiae</i> ," <i>J Biol Chem</i> , 267(23):16417-16423 (1992).
96.	D'Haeseleer, et al., "Genetic network inference: from co-expression clustering to reverse engineering," <i>Bioinformatics</i> , 16(8):707-726 (2000).

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U.S. Application No. 09/923,870

97.	Danchin, "Comparison Between the Escherichia coli and Bacillus subtilis Genomes Suggests That a Major Function of Polynucleotide Phosphorylase is to Synthesize CDP," <u>DNA Research</u> , 4(1):9-18 (1997).
98.	Dandekar, et al., "Pathway Alignment: Application to the Comparative Analysis of Glycolytic Enzymes," <u>Biochem J</u> , 343(Pt 1):115-124 (1999).
99.	Dantigny, et al., "A new control strategy for yeast production based on the L/A* approach," <u>Appl Microbiol Biotechnol</u> , 36:352-357 (1991).
100.	Datsenko, KA and Wanner, BL, "One-step inactivation of chromosomal genes in <i>Escherichia coli</i> K-12 using PCR products," <u>Proc Natl Acad Sci U.S.A.</u> , 97(12):6640-6645 (2000).
101.	Daum, et al., "Biochemistry, cell biology and molecular biology of lipids of <i>Saccharomyces cerevisiae</i> ," <u>Yeast</u> , 14(16):1471-1510 (1998).
102.	Daum, et al., "Systematic analysis of yeast strains with possible defects in lipid metabolism," <u>Yeast</u> , 15(7):601-614 (1999).
103.	Dauner, et al., " <i>Bacillus subtilis</i> Metabolism and Energetics in Carbon-Limited and Excess-Carbon Chemostat Culture," <u>J Bacteriol</u> , 183(24):7308-7317 (2001).
104.	Dauner, et al., "Metabolic Flux Analysis with a Comprehensive Isotopomer Model in <i>Bacillus subtilis</i> ," <u>Biotechnol Bioeng</u> , 76(2):144-156 (2001).
105.	Dauner, M and Sauer, U, "Stoichiometric Growth Model for Riboflavin-Producing <i>Bacillus subtilis</i> ," <u>Biotechnol Bioeng</u> , 76(1):132-143 (2001).
106.	de Jong, H., "Modeling and simulation of genetic regulatory systems: a literature review," <u>J Comput Biol</u> , 9(1):67-103 (2002).
107.	De Reuse, et al., "The <i>Helicobacter pylori</i> ureC gene codes for a phosphoglucosamine mutase," <u>J Bacteriol</u> , 179(11):3488-3493 (1997).
108.	Delgado and Liao, "Identifying Rate-Controlling Enzymes in Metabolic Pathways without Kinetic Parameters," <u>Biotechnol Prog</u> , 7:15-20 (1991).
109.	Demain, et al., "Cellulase, clostridia, and ethanol," <u>Microbiol Mol Biol Rev</u> , 69(1):124-154 (2005).
110.	Department of Energy, <u>Breaking the Biological Barriers to Cellulosic Ethanol</u> (2006).
111.	DeRisi, et al., "Exploring the Metabolic and Genetic Control of Gene Expression on a Genomic Scale," <u>Science</u> , 278(5338):680-686 (1997).
112.	Devine, KM, "The <i>Bacillus subtilis</i> Genome Project: Aims and Progress," <u>Trends Biotechnol</u> , 13(6):210-216 (1995).
113.	Dickson, "Sphingolipid Functions in <i>Saccharomyces Cerevisiae</i> : Comparison to Mammals," <u>Annu Rev Biochem</u> , 67:27-48 (1998).
114.	Dickson, et al., "Serine palmitoyltransferase," <u>Methods Enzymol</u> , 311:3-9 (2000).
115.	DiRusso, CC and Black, PN, "Long-chain fatty acid transport in bacteria and yeast. Paradigms for defining the mechanism underlying this protein-mediated process," <u>Mol Cell Biochem</u> , 192(1-2):41-52 (1999).
116.	
117.	Edwards, et al., "Characterizing the Metabolic Phenotype: A Phenotype Phase Plane Analysis," <u>Biotech Bioeng</u> , 77(1):27-36 (2002).
118.	Edwards, et al., "In Silico Predictions of <i>Escherichia coli</i> metabolic capabilities are Consistent with Experimental Data," <u>Nat Biotechnol</u> , 19(2):125-130 (2001).
119.	Edwards, JS and Palsson, BO, "Robustness analysis of the <i>Escherichia coli</i> metabolic network," <u>Biotechnol Prog</u> , 16(6):927-939 (2000).

EXHIBIT A
U.S. Application No. 09/923,870

120.	Edwards, JS, and Palsson, BO, "Metabolic flux balance analysis and the <i>in silico</i> analysis of Escherichia coli K-12 gene deletions," <u>BMC Bioinformatics</u> , 1:1-10 (2000).
121.	Eisen, et al., "Cluster analysis and display of genome-wide expression patterns," <u>Proc Natl Acad Sci U.S.A.</u> , 95:14863-14868 (1998).
122.	Eisenberg, et al., "Protein Function in the Post-Genomic Era," <u>Nature</u> , 405(6788):823-826 (2000).
123.	Ermolaeva, et al., "Prediction of Operons in Microbial Genomes," <u>Nucl Acids Research</u> , 29(5):1216-1221 (2001).
124.	
125.	Fiehn, "Metabolomics--the link between genotypes and phenotypes," <u>Plant Mol Biol</u> , 48(1-2):155-171 (2002).
126.	Finel, "Does NADH play a central role in energy metabolism in Helicobacter pylori?," <u>Trends Biochem Sci</u> , 23(11):412-413 (1998).
127.	Fiorelli, et al., "Chronic non-spherocytic haemolytic disorders associated with glucose-6-phosphate dehydrogenase variants," <u>Bailliere's Clinical Haematology</u> , 13:39-55 (2000).
128.	
129.	Flikweert, et al., "Pyruvate decarboxylase: an indispensable enzyme for growth of <i>Saccharomyces cerevisiae</i> on glucose," <u>Yeast</u> , 12(3):247-257 (1996).
130.	Forst, "Network genomics-- A Novel approach for the analysis of biological systems in the post-genomic era," <u>Molecular Biology Reports</u> , 29(3):265-280 (2002).
131.	Forster, et al., "Large-scale evaluation of <i>in silico</i> gene deletions in <i>Saccharomyces cerevisiae</i> ," <u>Omics</u> , 7(2):193-202 (2003).
132.	Fraenkel, "The accumulation of glucose 6-phosphate from glucose and its effect in an Escherichia coli mutant lacking phosphoglucose isomerase and glucose 6-phosphate dehydrogenase," <u>J Biol Chem</u> , 243(24):6451-6457 (1968).
133.	Fraser, et al., "Microbial genome sequencing," <u>Nature</u> , 406:799-803 (2000).
134.	Fromont-Racine, et al., "Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens," <u>Nat Genet</u> , 16(3):277-282 (1997).
135.	Fukuchi, et al., "Isolation, overexpression and disruption of a <i>Saccharomyces cerevisiae</i> YNK gene encoding nucleoside diphosphate kinase," <u>Gene</u> , 129(1):141-146 (1993).
136.	Gaasterland, T. and Selkov, E., "Reconstruction of Metabolic Networks Using Incomplete Information," <u>Proc Int Conf Intell Syst Mol Biol</u> , 3:127-135 (1995).
137.	Gancedo, C and Delgado, MA, "Isolation and characterization of a mutant from <i>Saccharomyces cerevisiae</i> lacking fructose 1,6-bisphosphatase," <u>Eur J Biochem</u> , 139:651-655 (1984).
138.	Gangloff, et al., "Molecular cloning of the yeast mitochondrial aconitase gene (ACO1) and evidence of a synergistic regulation of expression by glucose plus glutamate," <u>Mol Cell Biol</u> , 10(7):3551-3561 (1990).
139.	
140.	Glasner, et al., "ASAP, a systematic annotation package for community analysis of genomes," <u>Nucleic Acids Res</u> , 31(1):147-151 (2003).
141.	Goffeau, A, "Four years of post-genomic life with 6000 yeast genes," <u>FEBS Lett</u> , 480(1):37-41 (2000).
142.	Goryanin, et al., "Mathematical simulation and analysis of cellular metabolism and regulation," <u>Bioinformatics</u> , 15(9):749-758 (1999).

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U.S. Application No. 09/923,870

143.	Goto, et al., "LIGAND database for enzymes, compounds and reactions," <u>Nucleic Acids Res</u> , 27(1):377-379 (1999).
144.	Goto, et al., "LIGAND: chemical database for enzyme reactions," <u>Bioinformatics</u> , 14(7):591-599 (1998).
145.	Grewal, et al., "Computer Modelling of the Interaction Between Human Choriogonadotropin and Its Receptor," <u>Protein Engineering</u> , 7(2):205-211 (1994).
146.	Griffin, et al., "Complementary profiling of gene expression at the transcriptome and proteome levels in <i>Saccharomyces cerevisiae</i> ," <u>Mol Cell Proteomics</u> , 1:323-333 (2002).
147.	Grundy, et al., "Regulation of the <i>Bacillus subtilis</i> acetate kinase gene by CcpA," <u>J Bacteriol</u> , 175(22):7348-7355 (1993).
148.	Guelzim, et al., "Topological and causal structure of the yeast transcriptional regulatory network," <u>Nat Genet</u> , 31(1):60-63 (2002).
149.	Guetsova, et al., "The isolation and characterization of <i>Saccharomyces cerevisiae</i> mutants that constitutively express purine biosynthetic genes," <u>Genetics</u> , 147(2):383-397 (1997).
150.	
151.	Hardison, et al., "Globin Gene Server: A Prototype E-Mail Database Server Featuring Extensive Multiple Alignments and Data Compilation for Electronic Genetic Analysis," <u>Genomics</u> , 21(2):344-353 (1994).
152.	Hartig, et al., "Differentially regulated malate synthase genes participate in carbon and nitrogen metabolism of <i>S. cerevisiae</i> ," <u>Nucleic Acids Res</u> , 20(21):5677-5686 (1992).
153.	Hasty, et al., "Computational Studies of Gene Regulatory Networks: <i>In Numero</i> Molecular Biology," <u>Nat Rev Genet</u> , 2(4):268-279 (2001).
154.	Hata, et al., "Characterization of a <i>Saccharomyces cerevisiae</i> mutant, N22, defective in ergosterol synthesis and preparation of [28- ¹⁴ C]ergosta-5,7-dien-3 beta-ol with the mutant," <u>J Biochem</u> , 94(2):501-510 (1987).
155.	Hatzimanikatis, et al., "Analysis and Design of Metabolic Reaction Networks Via Mixed-Integer linear Optimization," <u>AIChE Journal</u> , 42(5):1277-1292 (1996).
156.	Hazell, et al., "How <i>Helicobacter pylori</i> works: an overview of the metabolism of <i>Helicobacter pylori</i> ," <u>Helicobacter</u> , 2(1):1-12 (1997).
157.	Heijnen, et al., "Application of balancing methods in modeling the penicillin fermentation," <u>Biotechnology & Bioeng.</u> , 21:2175-2201 (1979).
158.	Heinisch, et al., "Investigation of two yeast genes encoding putative isoenzymes of phosphoglycerate mutase," <u>Yeast</u> , 14(3):203-213 (1998).
159.	Heinrich, et al., "Metabolic regulation and mathematical models," <u>Prog Biophys Mol Biol</u> , 32(1):1-82 (1977).
160.	Heinrich, et al., "Stoichiometric Analysis," <u>The Regulation of Cellular Systems</u> , xix:75-111 and 372, Chapman & Hall, New York (1996).
161.	Henriksen, et al., "Growth energetics and metabolism fluxes in continuous cultures of <i>Penicillium chrysogenum</i> ," <u>J of Biotechnol</u> , 45(2):149-164 (1996).
162.	Heyer, et al., "Exploring expression data: identification and analysis of coexpressed genes," <u>Genome Res</u> , 9(11):1106-1115 (1999).
163.	Holter, et al., "Dynamic modeling of gene expression data," <u>Proc Natl Acad Sci U.S.A.</u> , 98(4):1693-1698 (2001).
164.	Holter, et al., "Fundamental patterns underlying gene expression profiles: simplicity from complexity," <u>Proc Natl Acad Sci U.S.A.</u> , 97:8409-8414 (2000).
165.	Houghten, "Generation and use of synthetic peptide combinatorial libraries for basic research and drug discovery," <u>Nature</u> , 354(6348):84-86 (1991).

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U.S. Application No. 09/923,870

166.	Hughes, et al., "Functional discovery via a compendium of expression profiles," <u>Cell</u> , 102(1):109-126 (2000).
167.	Hughes, et al., "Helicobacter pylori porCDAB and oodABC genes encode distinct pyruvate: flavodoxin and 2-oxoglutarate:acceptor oxidoreductases which mediate electron transport to NADP," <u>J Bacteriol</u> , 180(5):1119-1128 (1998).
168.	Nekyer, et al., "Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network," <u>Science</u> , 292(5518):929-934 (2001).
169.	Ince, IE and Knowles, CJ, "Ethylene formation by cell-free extracts of <i>Escherichia coli</i> ," <u>Arch Microbiol</u> , 146(2):151-158 (1986).
170.	Ishii, et al., "DBTBS: a database of <i>Bacillus subtilis</i> promoters and transcription factors," <u>Nucleic Acids Res</u> , 29(1):278-280 (2001).
171.	Iyer, et al., "Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF," <u>Nature</u> , 409(6819):533-538 (2001).
172.	Jamshidi, et al., "Dynamic simulation of the human red blood cell metabolic network," <u>Bioinformatics</u> , 17(3):286-287 (2001).
173.	Jamshidi, et al., "In silico model-driven assessment of the effects of single nucleotide polymorphisms (SNPs) on human red blood cell-metabolism," <u>Genome Research</u> , 12(11):1687-1692 (2002).
174.	Jenkins, LS and Nunn, WD, "Genetic and molecular characterization of the genes involved in short-chain fatty acid degradation in <i>Escherichia coli</i> : the ato system," <u>J Bacteriol</u> , 169(1):42-52 (1987).
175.	Jenssen, et al., "A Literature Network of Human Genes for High-Throughput Analysis of Gene Expression," <u>Nat Genet</u> , 28(1):21-28 (2001).
176.	Jorgensen, et al., "Metabolic flux distributions in <i>Penicillium chrysogenum</i> during fed-batch cultivations," <u>Biotechnol Bioeng</u> , 46(2):117-131 (1995).
177.	Joshi, A and Palsson, BO, "Metabolic dynamics in the human red cell. Part I--A comprehensive kinetic model," <u>J Theor Biol</u> , 141(4):515-528 (1989).
178.	Juty, et al., "Simultaneous Modeling of Metabolic, Genetic, and Product-Interaction Networks," <u>Briefings in Bioinformatics</u> , 2(3):223-233 (2001).
179.	Kanehisa, M and Goto, S, "Kyoto Encyclopedia of Genes and Genomes database (KEGG)," <u>Nucleic Acids Res</u> , 28(1):27-30 (2000).
180.	Karp, "An ontology for biological function based on molecular interactions," <u>Bioinformatics</u> , 16(3):269-285 (2000).
181.	Karp, et al., "EcoCyc: encyclopedia of <i>Escherichia coli</i> genes and metabolism," <u>Nucleic Acids Res</u> , 27(1):55-58 (1999).
182.	Karp, et al., "HinCyc: A knowledge base of the complete genome and metabolic pathways of <i>H. influenzae</i> ," <u>Proc Int Conf Intell Syst Mol Biol</u> , 4:116-124 (1996).
183.	Karp, et al., "Integrated pathway-genome databases and their role in drug discovery," <u>Trends Biotechnol</u> , 17(7):275-281 (1999).
184.	Karp, et al., "The EcoCyc and MetaCyc databases," <u>Nucleic Acids Research</u> , 28(1):56-59 (2000).
185.	Kather, et al., "Another unusual type of citric acid cycle enzyme in <i>Helicobacter pylori</i> : the malate:quinone oxidoreductase," <u>J Bacteriol</u> , 182(11):3204-3209 (2000).
186.	Keating, et al., "An ethanologenic yeast exhibiting unusual metabolism in the fermentation of lignocellulosic hexose sugars," <u>J Ind Microbiol Biotechnol</u> , 31(5):235-244 (2004).
187.	

EXHIBIT A
U.S. Application No. 09/923,870

188.	Kim, et al., " <i>Saccharomyces cerevisiae</i> contains two functional citrate synthase genes.," <i>Mol Cell Biol</i> , 6(6):1936-1942 (1986).
189.	Kirkman, et al., "Red cell NADP+ and NADPH in glucose-6-phosphate dehydrogenase deficiency," <i>Journal of Clinical Investigation</i> , 55(4):875-878 (1975).
190.	Kremling, et al., "The organization of metabolic reaction networks. III. Application for diauxic growth on glucose and lactose," <i>Metab Eng</i> , 3(4):362-379 (2001).
191.	Kunst, et al., "The Complete Genome Sequence of the Gram-positive Bacterium <i>Bacillus subtilis</i> ," <i>Nature</i> , 390(6557):249-256 (1997).
192.	Lacroute, "Regulation of pyrimidine biosynthesis in <i>Saccharomyces cerevisiae</i> ," <i>J Bacteriol</i> , 95(3):824-832 (1968).
193.	Latif, F and Rajoka, MI, "Production of ethanol and xylitol from corn cobs by yeasts," <i>Bioresour Technol</i> , 77(1):57-63 (2001).
194.	Lendenmann, U and Egli, T, "Is <i>Escherichia coli</i> growing in glucose-limited chemostat culture able to utilize other sugars without lag?," <i>Microbiology</i> , 141(Pt 1):71-78 (1995).
195.	Leyva-Vasquez, MA and Setlow, P, "Cloning and nucleotide sequences of the genes encoding triose phosphate isomerase, phosphoglycerate mutase, and enolase from <i>Bacillus subtilis</i> ," <i>J Bacteriol</i> , 176(13):3903-3910 (1994).
196.	Li, C and Wong, WH, "Model-based analysis of oligonucleotide arrays: expression index computation and outlier detection," <i>Proc Natl Acad Sci U.S.A.</i> , 98(1):31-36 (2001).
197.	Liao, et al., "Pathway Analysis, Engineering, and Physiological Considerations for Redirecting Central Metabolism," <i>Biotechnol Bioeng</i> , 52(1):129-140 (1996).
198.	Liao, JC and Oh, MK, "Toward predicting metabolic fluxes in metabolically engineered strains," <i>Metab Eng</i> , 1(3):214-223 (1999).
199.	Link, et al., "Methods for generating precise deletions and insertions in the genome of wild-type <i>Escherichia coli</i> : Application to open reading frame characterization," <i>J Bacteriol</i> , 179(20):6228-6237 (1997).
200.	Loftus, et al., "Isolation, characterization, and disruption of the yeast gene encoding cytosolic NADP-specific isocitrate dehydrogenase," <i>Biochemistry</i> , 33(32):9661-9667 (1994).
201.	Lopez, et al., "The yeast inositol monophosphatase is a lithium- and sodium-sensitive enzyme encoded by a non-essential gene pair," <i>Mol Microbiol</i> , 31(4):1255-1264 (1999).
202.	
203.	Maier, et al., "Hydrogen uptake hydrogenase in <i>Helicobacter pylori</i> ," <i>FEMS Microbiol Lett</i> , 141(1):71-76 (1996).
204.	Marcelli, et al., "The respiratory chain of <i>Helicobacter pylori</i> : identification of cytochromes and the effects of oxygen on cytochrome and menaquinone levels," <i>FEMS Microbiol Lett</i> , 138(1):59-64 (1996).
205.	
206.	McAdams, HH and Arkin, A, "Simulation of Prokaryotic Genetic Circuits," <i>Annual Review of Biophysics and Biomolecular Structure</i> , 27:199-224 (1998).
207.	
208.	McAlister-Henn, L and Thompson, LM, "Isolation and expression of the gene encoding yeast mitochondrial malate dehydrogenase," <i>J Bacteriol</i> , 169(11):5157-5166 (1987).
209.	McGee, D.J., "Helicobacter pylori rocF is required for arginase activity and acid protection in vitro but is not essential for colonization of mice or for urease activity," <i>J Bacteriol</i> , 165(1):65-76 (1998).

EXHIBIT A
U.S. Application No. 09/923,870

210.	Meldrum, "Automation for genomics, part one: preparation for sequencing," <u>Genome Res.</u> 10(8):1081-1092 (2000).
211.	Mendes, P and Kell, D, "Non-linear optimization of biochemical pathways: Applications to metabolic engineering and parameter estimation," <u>Bioinformatics</u> , 14(10):869-883 (1998).
212.	Mendz, et al., "Characterisation of glucose transport in <i>Helicobacter pylori</i> ," <u>Biochim Biophys Acta</u> , 1244(2-3):269-276 (1995).
213.	Mendz, et al., "Characterization of fumarate transport in <i>Helicobacter pylori</i> ," <u>J Membr Biol</u> , 165(1):65-76 (1998).
214.	Mendz, et al., "De novo synthesis of pyrimidine nucleotides by <i>Helicobacter pylori</i> ," <u>J Appl Bacteriol</u> , 77(1):1-8 (1994).
215.	
216.	
217.	Mendz, et al., "In situ characterization of <i>Helicobacter pylori</i> arginase," <u>Biochim Biophys Acta</u> , 1388(2):465-477 (1998).
218.	Mendz, et al., "Purine metabolism and the microaerophily of <i>Helicobacter pylori</i> ," <u>Arch Microbiol</u> , 168(6):448-456 (1997).
219.	Mendz, et al., "The Entner-Doudoroff pathway in <i>Helicobacter pylori</i> ," <u>Arch Biochem Biophys</u> , 312(2):349-356 (1994).
220.	Mendz, GL and Hazell SL, "Amino acid utilization by <i>Helicobacter pylori</i> ," <u>Int J Biochem Cell Biol</u> , 27(10):1085-1093 (1995).
221.	
222.	Mendz, GL and Hazell, SL, "Glucose phosphorylation in <i>Helicobacter pylori</i> ," <u>Arch Biochem Biophys</u> , 300(1):522-525 (1993).
223.	Mendz, GL, et al., "Pyruvate metabolism in <i>Helicobacter pylori</i> ," <u>Arch Microbiol</u> , 162(3):187-192 (1994).
224.	
225.	Mewes, et al., "MIPS: A database for genomes and protein sequences," <u>Nucleic Acids Research</u> , 30(1):31-34 (2002).
226.	Mitchell, "The GLN1 locus of <i>Saccharomyces cerevisiae</i> encodes glutamine synthetase," <u>Genetics</u> , 111(2):243-258 (1985).
227.	Moszer, "The Complete Genome of <i>Bacillus Subtilis</i> : From Sequence Annotation to Data Management and Analysis," <u>FEBS Lett</u> , 430(1-2):28-36 (1998).
228.	Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," <u>Nucleic Acids Res.</u> 30(1):62-65 (2002).
229.	Mulquinney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," <u>Biochem J</u> , 342(Pt 3):597-604 (1999).
230.	Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inositol monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," <u>Mol Microbiol</u> , 36(3):651-661 (2000).
231.	Nedenskov, "Nutritional requirements for growth of <i>Helicobacter pylori</i> ," <u>Appl Environ Microbiol</u> , 60(9):3450-3453 (1994).
232.	Nissen, et al., "Expression of a cytoplasmic transhydrogenase in <i>Saccharomyces cerevisiae</i> results in formation of 2-oxoglutarate due to depletion of the NADPH pool," <u>Yeast</u> , 18(1):19-32 (2001).
233.	Nissen, et al., "Flux distributions in anaerobic, glucose-limited continuous cultures of <i>Saccharomyces cerevisiae</i> ," <u>Microbiology</u> , 143(Pt 1):203-218 (1997).

EXHIBIT A
U.S. Application No. 09/923,870

234.	Ogasawara, "Systematic function analysis of <i>Bacillus subtilis</i> genes," <i>Res Microbiol</i> , 151(2):129-134 (2000).
235.	Ogata, et al., "KEGG: Kyoto Encyclopedia of Genes and Genomes," <i>Nucleic Acids Res</i> , 27(1):29-34 (1999).
236.	Oh, MK and Liao, JC, "Gene expression profiling by DNA microarrays and metabolic fluxes in <i>Escherichia coli</i> ," <i>Biotech Prog</i> , 16:278-286 (2000).
237.	Olsson, et al., "Separate and simultaneous enzymatic hydrolysis and fermentation of wheat hemicellulose with recombinant xylose utilizing <i>Saccharomyces cerevisiae</i> ," <i>Appl Biochem Biotechnol</i> , 129-132:117-129 (2006).
238.	Otto, et al., "A mathematical model for the influence of fructose 6-phosphate, ATP, potassium, ammonium and magnesium on the phosphofructokinase from rat erythrocytes," <i>Eur J Biochem</i> , 49(1):169-178 (1974).
239.	Ouzounis, CA and Karp, PD, "Global Properties of the Metabolic Map of <i>Escherichia coli</i> ," <i>Genome Res</i> , 10(4):568-576 (2000).
240.	Overbeek, et al., "WIT: Integrated System for High-Throughput Genome Sequence Analysis and Metabolic Reconstruction" <i>Nucleic Acids Res</i> , 28(1):123-125 (2000).
241.	Overkamp, et al., "In vivo analysis of the mechanisms for oxidation of cytosolic NADH by <i>Saccharomyces cerevisiae</i> mitochondria," <i>J Bacteriol</i> , 182(10):2823-2830 (2000).
242.	Ozcan, S., Freidel, K., Leuker, A. & Ciriacy, M., "Glucose uptake and catabolite repression in dominant HTR1 mutants of <i>Saccharomyces cerevisiae</i> ," <i>J Bacteriol</i> , 175(17):5520-5528 (1993).
243.	Pallotta, et al., "Saccharomyces cerevisiae mitochondria can synthesise FMN and FAD from externally added riboflavin and export them to the extramitochondrial phase," <i>FEBS Lett</i> , 428(3):245-249 (1998).
244.	Palmieri, et al., "Identification and function of new transporters in yeast mitochondria," <i>Biochim Biophys Acta</i> , 1459(2-3):363-369 (2000).
245.	Palmieri, et al., "Identification of the yeast ACR1 gene product as a succinate-fumarate transporter essential for growth on ethanol or acetate," <i>FEBS Lett</i> , 417(1):114-118 (1997).
246.	Palmieri, et al., "Identification of the yeast mitochondrial transporter for oxaloacetate and sulfate," <i>J Biol Chem</i> , 274(32):22184-22190 (1999).
247.	Palmieri, et al., "Yeast mitochondrial carriers: bacterial expression, biochemical identification and metabolic significance," <i>J Bioenerg Biomembr</i> , 32(1):67-77 (2000).
248.	Palsson, "The Challenges of in Silico Biology," <i>Nat Biotechnol</i> , 18(11):1147-1150 (2000).
249.	Papin, et al., "The genome-scale metabolic extreme pathway structure in <i>Haemophilus influenzae</i> shows significant network redundancy," <i>J Theor Biol</i> , 215(1):67-82 (2002).
250.	Parks, "Metabolism of sterols in yeast," <i>CRC Crit Rev Microbiol</i> , 6(4):301-341 (1978).
251.	Parks, et al., "Use of sterol mutants as probes for sterol functions in the yeast <i>Saccharomyces cerevisiae</i> ," <i>Crit Rev Biochem Mol Biol</i> , 34(6):399-404 (1999).
252.	
253.	Paulsen, et al., "Unified inventory of established and putative transporters encoded within the complete genome of <i>Saccharomyces cerevisiae</i> ," <i>FEBS Lett</i> , 430(1-2):116-125 (1998).
254.	Pearson, et al., "Comparison of DNA Sequences With Protein Sequences," <i>Genomics</i> , 46(1):24-36 (1997).
255.	Persson, et al., "Phosphate permeases of <i>Saccharomyces cerevisiae</i> : structure, function and regulation," <i>Biochim Biophys Acta</i> , 1422(3):255-272 (1999).

EXHIBIT A
U.S. Application No. 09/923,870

256.	Peterson, et al., "The Comprehensive Microbial Resource," <i>Nucleic Acids Res</i> , 29(1):123-125 (2001).
257.	Pharkya, et al., "Exploring the overproduction of amino acids using the bilevel optimization framework OptKnock," <i>Biotechnol Bioeng</i> , 84(7):887-899 (2003).
258.	Phelps, et al., "Metabolomics and microarrays for improved understanding of phenotypic characteristics controlled by both genomics and environmental constraints," <i>Curr Opin Biotechnol</i> , 13(1):20-24 (2002).
259.	Pitson, et al., "The tricarboxylic acid cycle of <i>Helicobacter pylori</i> ," <i>Eur J Biochem</i> , 260(1):258-267 (1999).
260.	Price, et al., "Determination of redundancy and systems properties of the metabolic network of <i>Helicobacter pylori</i> using genome-scale extreme pathway analysis," <i>Genome Res</i> , 12(5):760-769 (2002).
261.	Price, et al., "Genome-scale models of microbial cells: evaluating the consequences of constraints," <i>Nat Rev Microbiol</i> , 2(11):886-897 (2004).
262.	Price, et al., "Network-based analysis of metabolic regulation in the human red blood cell," <i>J Theor Biol</i> , 223(2):185-194 (2003).
263.	Przybyla-Zawislak, et al., "Genes of succinyl-CoA ligase from <i>Saccharomyces cerevisiae</i> ," <i>Eur J Biochem</i> , 258(2):736-743 (1998).
264.	Qian, et al., "Ethanol production from dilute-Acid softwood hydrolysate by co-culture," <i>Appl Biochem Biotechnol</i> , 134(3):273-284 (2006).
265.	Reed, et al., "An expanded genome-scale model of <i>Escherichia coli</i> K-12 (iJR904 GSM/GPR)," <i>Genome Biol</i> , 4(9):R54 (2003).
266.	Reed, JL and Palsson, BO, "Thirteen years of building constraint-based in silico models of <i>Escherichia coli</i> ," <i>J Bacteriol</i> , 185(9):2692-2699 (2003).
267.	Regenberg, et al., "Substrate specificity and gene expression of the amino-acid permeases in <i>Saccharomyces cerevisiae</i> ," <i>Curr Genet</i> , 36(6):317-328 (1999).
268.	Remize, et al., "Engineering of the pyruvate dehydrogenase bypass in <i>Saccharomyces cerevisiae</i> : role of the cytosolic Mg(2+) and mitochondrial K(+) acetaldehyde dehydrogenases Ald6p and Ald4p in acetate formation during alcoholic fermentation," <i>Appl Environ Microbiol</i> , 66(8):2151-2159 (2000).
269.	Ren, et al., "Genome-wide location and function of DNA binding proteins," <i>Science</i> , 290(5500):2306-2309 (2000).
270.	Repetto, B and Tzagoloff, A, "In vivo assembly of yeast mitochondrial alpha-ketoglutarate dehydrogenase complex," <i>Mol Cell Biol</i> , 11(8):3931-3939 (1991).
271.	Reynolds, DJ and Ponn, CW, "Characteristics of <i>Helicobacter pylori</i> growth in a defined medium and determination of its amino acid requirements," <i>Microbiology</i> , 140(Pt 10):2649-2656 (1994).
272.	Rhee, et al., "Activation of gene expression by a ligand-induced conformational change of a protein-DNA complex," <i>J Biol Chem</i> , 273(18):11257-11266 (1998).
273.	Romero, PR and Karp, P, "Nutrient-Related Analysis of Pathway/Genome Databases," <i>Pac Symp Biocomput</i> , 471-482 (2001).
274.	Saier, MH, "Genome sequencing and informatics: new tools for biochemical discoveries," <i>Plant Physiol</i> , 117(4):1129-1133 (1998).
275.	Salgado, et al., <i>Nucleic Acids Res</i> , 29(1):72-74 (2001).
276.	Salmon, et al., "Global gene expression profiling in <i>Escherichia coli</i> K12. The effects of oxygen availability and FNR," <i>J Biol Chem</i> , 278(32):29837-29855 (2003).
277.	Sauer, et al., "Metabolic flux ratio analysis of genetic and environmental modulations of <i>Escherichia coli</i> central carbon metabolism," <i>J Bacteriol</i> , 181(21):6679-6688 (1999).

EXHIBIT A
U.S. Application No. 09/923,870

278.	Sauer, U and Bailey, JE, "Estimation of P-to-O Ratio in <i>Bacillus subtilis</i> and Its Influence on Maximum Riboflavin Yield," <i>Biotechnol Bioeng</i> , 64(6):750-754 (1999).
279.	Sauer, Uwe, "Evolutionary Engineering of Industrially Important Microbial Phenotypes," <i>Adv in Biochem Eng Biotechnol</i> , 73:129-169 (2001).
280.	Savageau, "Biochemical systems analysis. I. Some mathematical properties of the rate law for the component enzymatic reactions," <i>J Theor Biol</i> , 25(3):365-369 (1969).
281.	Schaeff-Gerstenschlager, I and Zimmermann, FK, "Pentose-phosphate pathway in <i>Saccharomyces cerevisiae</i> : analysis of deletion mutants for transketolase, transaldolase, and glucose 6-phosphate dehydrogenase," <i>Curr Genet</i> , 24(5):373-376 (1993).
282.	Schaff, et al., "the Virtual cell" <i>Proceedings of the Pacific Symposium on Biocomputing</i> , 4:228-239 (1999).
283.	
284.	Schilling, "On Systems Biology and the Pathway Analysis of Metabolic Networks," Department of Bioengineering, University of California, San Diego: La Jolla, p. 198-241 (2000).
285.	Schilling, CH and Palsson, BO, "Assessment of the Metabolic Capabilities of <i>Haemophilus influenzae</i> Rd Through a Genome-scale Pathway Analysis," <i>J Theor Biol</i> , 203(3):249-283 (2000).
286.	Schilling, CH and Palsson, BO, "The Underlying Pathway Structure of Biochemical Reaction Networks," <i>Proc Natl Acad Sci U.S.A.</i> , 95(8):4193-4198 (1998).
287.	Schilling, et al., "Combining Pathway Analysis with Flux Balance Analysis for the Comprehensive Study of Metabolic Systems," <i>Biotechnol Bioeng</i> , 71(4):286-306 (2000-2001).
288.	Schilling, et al., "Genome-scale metabolic model of <i>Helicobacter pylori</i> 26695," <i>J Bacteriol</i> , 184(16):4582-4593 (2002).
289.	Schilling, et al., "Metabolic Pathway Analysis: Basic Concepts and Scientific Applications in the Post-genomic Era," <i>Biotechnol Prog</i> , 15(3):296-303 (1999).
290.	Schilling, et al., "Theory for the Systematic Definition of Metabolic Pathways and Their Use in Interpreting Metabolic Function from a Pathway-Oriented Perspective," <i>J Theor Biol</i> , 203(3):229-248 (2000).
291.	Schneider, et al., "The <i>Escherichia coli</i> gabDTPC operon: specific gamma-aminobutyrate catabolism and nonspecific induction," <i>J Bacteriol</i> , 184(24):6976-6986 (2002).
292.	Schuster, et al., "A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks," <i>Nature Biotechnol</i> , 18(3):326-332 (2000).
293.	Schuster, et al., "Detection of elementary flux modes in biochemical networks: a promising tool for pathway analysis and metabolic engineering," <i>Trends Biotechnol</i> , 17(2):53-60 (1999).
294.	Schuster, et al., "Exploring the pathway structure of metabolism: decomposition into subnetworks and application to <i>Mycoplasma pneumoniae</i> ," <i>Bioinformatics</i> , 18(2):351-361 (2002).
295.	Schuster, S and Hilgetag, C, "On elementary flux modes in biochemical reaction systems at steady state," <i>J Biol Syst</i> , 2(2):165-182 (1994).
296.	Schwikowski, et al., "A network of protein-protein interactions in yeast," <i>Nature Biotechnol</i> , 18(12):1257-1261 (2000).
297.	
298.	

EXHIBIT A
U.S. Application No. 09/923,870

299.	Selkov, et al., "Functional Analysis of Gapped Microbial Genomes: Amino Acid Metabolism of <i>Thiobacillus Ferrooxidans</i> ," <u>Proc Natl Acad Sci U.S.A.</u> , 97(7):3509-3514 (2000).
300.	Selkov, et al., "MPW: the metabolic pathways database," <u>Nucleic Acids Res</u> , 26(1):43-45 (1998)
301.	Selkov, et al., "The metabolic pathway collection from EMP: the enzymes and metabolic pathways database," <u>Nucleic Acids Res</u> , 24(1):26-28 (1996).
302.	Shen Orr, et al., "Network motifs in the transcriptional regulation network of <i>Escherichia coli</i> ," <u>Nat Genet</u> , 31(1):64-68 (2002).
303.	
304.	
305.	Silve, et al., "The immunosuppressant SR 31747 blocks cell proliferation by inhibiting a steroid isomerase in <i>Saccharomyces cerevisiae</i> ," <u>Mol Cell Biol</u> , 16(6):2719-2727 (1996).
306.	Skouloubri, et al., "The <i>Helicobacter pylori</i> Urel protein is not involved in urease activity but is essential for bacterial survival in vivo," <u>Infect Immun</u> , 66(9):4517-4521 (1998).
307.	Smith, et al., "Functional analysis of the genes of yeast chromosome V by genetic footprinting," <u>Science</u> , 274(5295):2069-2074 (1996).
308.	
309.	
310.	Sorlie, et al., "Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications," <u>Proc Natl Acad Sci U.S.A.</u> , 98(19):10869-10874 (2001).
311.	Stark, et al., "Amino acid utilisation and degradation of glutamine and asparagine by <i>Helicobacter pylori</i> ," <u>J Med Microbiol</u> , 36(9):793-800 (1997).
312.	Stephanopoulos, "Metabolic engineering," <u>Curr Opin Biotechnol</u> , 5(2):196-200 (1994).
313.	Summers, et al., "Saccharomyces cerevisiae cho2 mutants are deficient in phospholipid methylation and cross-pathway regulation of inositol synthesis" <u>Genetics</u> , 120(4):909-922 (1988).
314.	Swartz, "A PURE approach to constructive biology," <u>Nat Biotechnol</u> , 19(8):732-733 (2001).
315.	Syvanen, "Accessing genetic variation: Genotyping single nucleotide polymorphisms," <u>Nat Rev Genet</u> , 2(12):930-942 (2001).
316.	Szambelan, et al., "Use of <i>Zymomonas mobilis</i> and <i>Saccharomyces cerevisiae</i> mixed with <i>Kluyveromyces fragilis</i> for improved ethanol production from Jerusalem artichoke tubers," <u>Biotechnol Lett</u> , 26(10):845-848 (2004).
317.	Tamayo, et al., "Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation," <u>Proc Natl Acad Sci U.S.A.</u> , 96(6):2907-2912 (1999).
318.	
319.	Taniguchi, M and Tanaka, T, "Clarification of interactions among microorganisms and development of co-culture system for production of useful substances," <u>Adv Biochem Eng Biotechnol</u> , 90:35-62 (2004).
320.	Tao, et al., "Engineering a homo-ethanol pathway in <i>Escherichia coli</i> : increased glycolytic flux and levels of expression of glycolytic genes during xylose fermentation," <u>J Bacteriol</u> , 183(10):2979-2988 (2001).

EXHIBIT A
U.S. Application No. 09/923,870

321.	ter Linde, et al., "Genome-wide transcriptional analysis of aerobic and anaerobic chemostat cultures of <i>Saccharomyces cerevisiae</i> ," <u>J Bacteriol</u> , 181(24):7409-7413 (1999).
322.	Thomas, "Boolean Formalization of Genetic Control Circuits," <u>J Theor Biol</u> , 42(3):563-585 (1973).
323.	Thomas, "Logical Analyses of Systems Comprising Feedback Loops," <u>J Theor Biol</u> , 73(4):631-656 (1978).
324.	Thomas, D and Surdin-Kerjan, Y, "Metabolism of sulfur amino acids in <i>Saccharomyces cerevisiae</i> ," <u>Microbiol Mol Biol Rev</u> , 61(4):503-532 (1997).
325.	Tomb, et al., "The complete genome sequence of the gastric pathogen <i>Helicobacter pylori</i> ," <u>Nature</u> , 388(6642):539-547 (1997).
326.	Trotter, et al., "A genetic screen for aminophospholipid transport mutants identifies the phosphatidylinositol 4-kinase, STT4p, as an essential component in phosphatidylserine metabolism," <u>J Biol Chem</u> , 273(21):13189-13196 (1998).
327.	Uetz, et al., "A comprehensive analysis of protein-protein interactions in <i>Saccharomyces cerevisiae</i> ," <u>Nature</u> , 403(6770):623-627 (2000).
328.	Van den Berg, MA and Greensma, HY, "ACS2, a <i>Saccharomyces cerevisiae</i> gene encoding acetyl-coenzyme A synthetase, essential for growth on glucose," <u>Eur J Biochem</u> , 231(3):704-713 (1995).
329.	van Dijken, et al., "Alcoholic fermentation by 'non-fermentative' yeasts," <u>Yeast</u> , 2(2):123-127 (1986).
330.	van Dijken, et al., "Kinetics of growth and sugar consumption in yeasts," <u>Antonie Van Leeuwenhoek</u> , 63(3-4):343-352 (1993).
331.	Vanrolleghem, et al., "Validation of a Metabolic Network for <i>Saccharomyces cerevisiae</i> Using Mixed Substrate Studies," <u>Biotechnol Prog</u> , 12(4):434-448 (1996).
332.	Varma, A and Palsson, BO, "Metabolic capabilities of <i>Escherichia coli</i> . II: Optimal Growth Patterns," <u>J Theor Biol</u> , 165:503-522 (1993).
333.	Varma, A and Palsson, BO, "Metabolic capabilities of <i>Escherichia coli</i> : I. Synthesis of Biosynthetic Precursors and Cofactors," <u>J Theor Biol</u> , 165:477-502 (1993).
334.	Varma, A and Palsson, BO, "Parametric sensitivity of stoichiometric flux balance models applied to wild-type <i>Escherichia coli</i> metabolism," <u>Biotechnol Bioeng</u> , 45(1):69-79 (1995).
335.	Varma, A and Palsson, BO, "Predictions for Oxygen Supply Control to Enhance Population Stability of Engineered Production Strains," <u>Biotechnol Bioeng</u> , 43(4):275-285 (1994).
336.	Varma, A and Palsson, BO, "Stoichiometric flux balance models quantitatively predict growth and metabolic by-product secretion in wild-type <i>Escherichia coli</i> W3110," <u>Appl Environ Microbiol</u> , 60(10):3724-3731 (1994).
337.	Varma, et al., "Biochemical Production Capabilities of <i>Escherichia coli</i> ," <u>Biotechnol Bioeng</u> , 42(1):59-73 (1993).
338.	Varma, et al., "Stoichiometric Interpretation of <i>Escherichia coli</i> Glucose Catabolism Under Various Oxygenation Rates," <u>Appl Environ Microbiol</u> , 59(8):2465-2473 (1993).
339.	Varner, J and Ramkrishna, D, "Mathematical Models of Metabolic Pathways," <u>Curr Opin Biotechnol</u> , 10(2):146-150 (1999).
340.	Velculescu, et al., "Analysing uncharted transcriptomes with SAGE," <u>Trends Genet</u> , 16(10):423-425 (2000).
341.	

EXHIBIT A
U.S. Application No. 09/923,870

342.	Verduyn, "Physiology of yeasts in relation to biomass yields," <u>Antonie Van Leeuwenhoek</u> , 60(3-4):325-353 (1991).
343.	Verduyn, et al., "A theoretical evaluation of growth yields of yeasts," <u>Antonie Van Leeuwenhoek</u> , 59(1):49-63 (1991).
344.	Verduyn, et al., "Energetics of <i>Saccharomyces cerevisiae</i> in anaerobic glucose-limited chemostat cultures," <u>J Gen Microbiol</u> , 136:405-412 (1990).
345.	Vissing, et al., "Paradoxically Enhanced Glucose Production During Exercise in Humans with Blocked Glycolysis Caused by Muscle Phosphofructokinase Deficiency," <u>Neurology</u> , 47(3):766-771 (1996).
346.	Wang, et al., "Computer-aided baker's yeast fermentations," <u>Biotechnol and Bioeng</u> , 19(1):69-86 (1977).
347.	Wang, et al., "Computer Control of Bakers' Yeast Production," <u>Biotechnol and Bioeng</u> , 21:975-995 (1979).
348.	
349.	Wen, et al., "Large-scale temporal gene expression mapping of central nervous system development," <u>Proc Natl Acad Sci U.S.A.</u> , 95(1):334-339 (1998).
350.	Wiback, SJ and Palsson, BO, "Extreme pathway analysis of human red blood cell metabolism," <u>Biophys J</u> , 83:808-818 (2002).
351.	Wieczorke, et al., "Concurrent knock-out of at least 20 transporter genes is required to block uptake of hexoses in <i>Saccharomyces cerevisiae</i> ," <u>FEBS Lett</u> , 464(3):123-128 (1999).
352.	
353.	Wingender, et al., "The TRANSFAC system on gene expression regulation," <u>Nucleic Acids Res</u> , 29(1):281-283 (2001).
354.	
355.	Wong, P., et al., "Mathematical Model of the Lac Operon: Inducer Exclusion, Catabolite Repression, and Diauxic Growth on Glucose and Lactose," <u>Biotechnol Prog</u> , 13(2):132-143 (1997).
356.	Yamada, et al., "Effects of common polymorphisms on the properties of recombinant human methylenetetrahydrofolate reductase," <u>Proc Natl Acad Sci U.S.A.</u> , 98(26):14853-14858 (2001).
357.	Yeung, et al., "Reverse engineering gene networks using singular value decomposition and robust regression," <u>Proc Natl Acad Sci U.S.A.</u> , 99(9):6163-6168 (2002).
358.	Yeung, et al., <u>Bioinformatics</u> , "Model-based clustering and data transformations for gene expression data," 17(10):977-87 (2001).
359.	Yoshida, et al., "Combined transcriptome and proteome analysis as a powerful approach to study genes under glucose repression in <i>Bacillus subtilis</i> ," <u>Nucleic Acids Res</u> , 29(3):686-692 (2001).
360.	Zanella, A and Bianchi, P, "Red cell pyruvate kinase deficiency: from genetics to clinical manifestations," <u>Bailliere's Best Pract Res Clin Haematol</u> 13(1):57-84 (2000)
361.	
362.	Zhu, J and Zhang, MO, "SCPD: a promoter database of the yeast <i>Saccharomyces cerevisiae</i> ," <u>Bioinformatics</u> , 15(7-8):607-611 (1999).
363.	
364.	Zweytick, et al., "Biochemical characterization and subcellular localization of the sterol C-24(28) reductase, erg4p, from the yeast <i>saccharomyces cerevisiae</i> ," <u>FEBS Lett</u> , 470(1):83-87 (2000).
365.	

EXHIBIT A
U.S. Application No. 09/923,870

366.	
367.	
368.	URL ca.expasy.org/sprot/ , protein database SWISS—PROT.
369.	
370.	URL dchip.org , dChip software.
371.	URL Dictionary.com pgs 1-2 (2004), Matrix.
372.	
373.	
374.	
375.	URL genome.ad.jp/kegg/ , Kyoto Encyclopedia of Genes and Genomes database (KEGG).
376.	URL Genome.jp Website, KEGG Bacillus subtilis, 1-7 (2005).
377.	
378.	
379.	
380.	
381.	
382.	URL ncbi.nlm.nih.gov/entrez/query.fcgi?db=Genome , The NCBI Entrez Genome database

all references duplicates of 6/18/09 IDS

/Russell S. Negin/

09/22/2009